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A.A. wolf range

0 55 110 220 330 440 Kilometers

Alexander Archipelago wolves

3rd ESA listing consideration

Management concerns:

- Habitat alteration
 - Effects on primary prey – deer
 - Effects on reproduction – den sites
- Harvest rates
- Genetic isolation

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Information Needed for Management

- Habitat selection
- Denning ecology
- Geographic variation in diets
- Predation patterns and foraging ecology
- Genetic structure
- Inbreeding

Photo: B. Dihle


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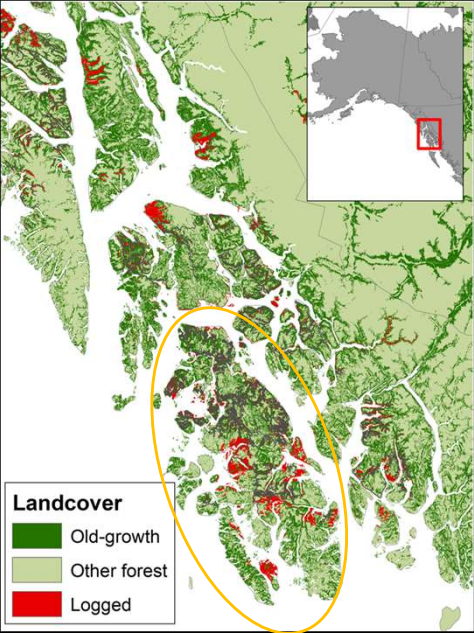
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Wolf Habitat Selection

Concerns focused on Prince of Wales Island

Logging → declines in deer habitat quality



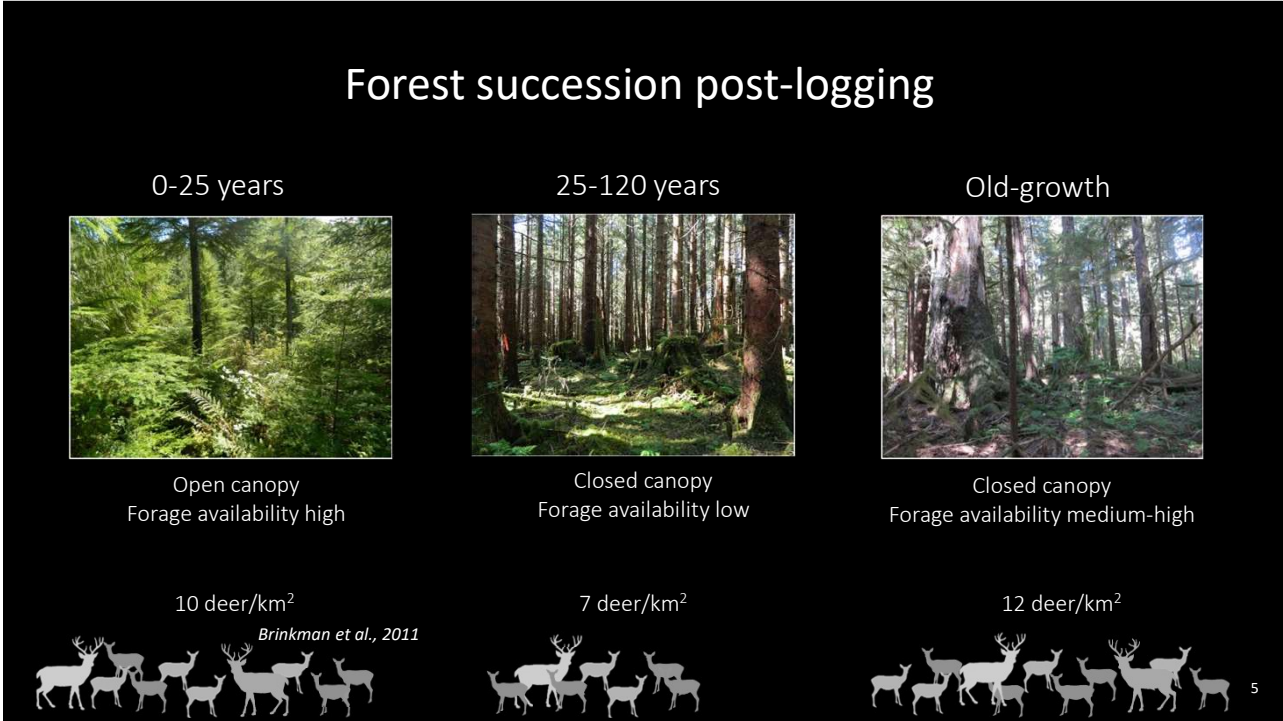


Landcover

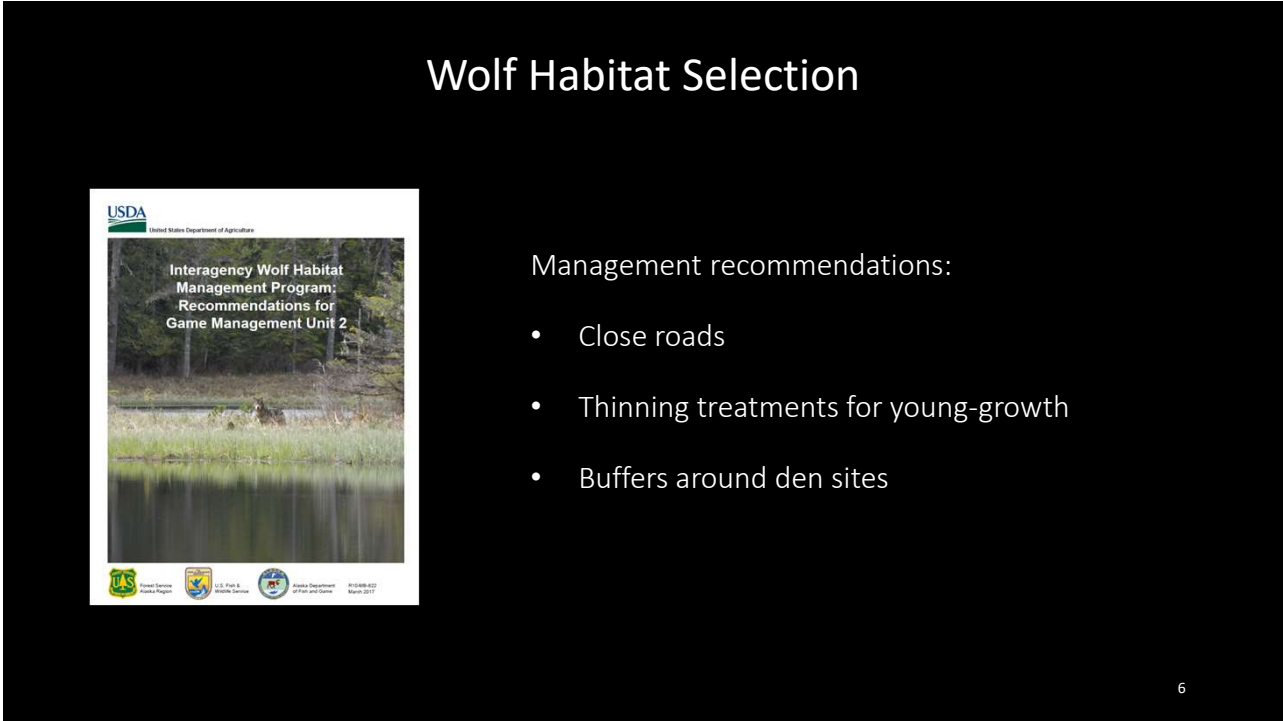
- Old-growth
- Other forest
- Logged

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Wolf Habitat Selection

- Avoided old clearcuts (>30 years)
- Selected young clearcuts (<30 years)
- Avoided thinned forest
- Avoided roads during summer
- Selected roads during winter
- Selected salmon habitat in the fall



Roffler, G. H. et al. 2018. Resource selection by coastal wolves reveals the seasonal importance of seral forest and suitable prey habitat. For. Ecol. Manage. 409: 190–201.

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Information Needed for Management

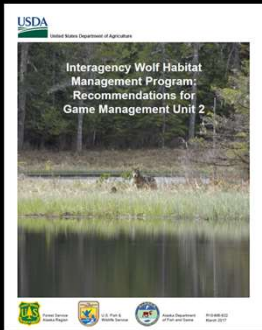
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Photo: B. Dihle

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Denning Ecology

Management recommendations:

- 1,200 ft (366 m) forested buffer
- Buffers required on all active and inactive dens



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Denning Ecology



Roffler, G. H., & Gregovich, D. P. 2018. Wolf space use during denning season on Prince of Wales Island, Alaska. Wildlife Biology, 2018. wlb.00468

- Den occupancy May 2nd – July 1st
- Core area smaller for breeding wolves vs. non-breeding wolves
- Minimum den buffer distance 734 m (2,408 ft)
- Half of occupied dens were from previously used sites

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Denning Ecology

Prey Species	Pups (Relative Frequency)	Adults (Relative Frequency)
deer	0.75	0.65
beaver	0.05	0.25
bird	0.05	0.05
mustelid	0.05	0.05
bear	0.05	0.05
other fish	0.02	0.02
microtine	0.02	0.02
domestic	0.02	0.02
salmon	0.02	0.02
marine mammal	0.02	0.02
amphibian	0.02	0.02

Roffler, G.H., et al. in press. Variation in adult and pup wolf diets at natal den sites is influenced by forest composition and configuration. Ecology and Evolution.

- Wolf pups ate more deer than adults
- Only 4 prey species detected in pups' diets
- Litter sizes highest in packs that ate the most deer
- Deer more vulnerable to predation in clearcuts and fragmented habitat

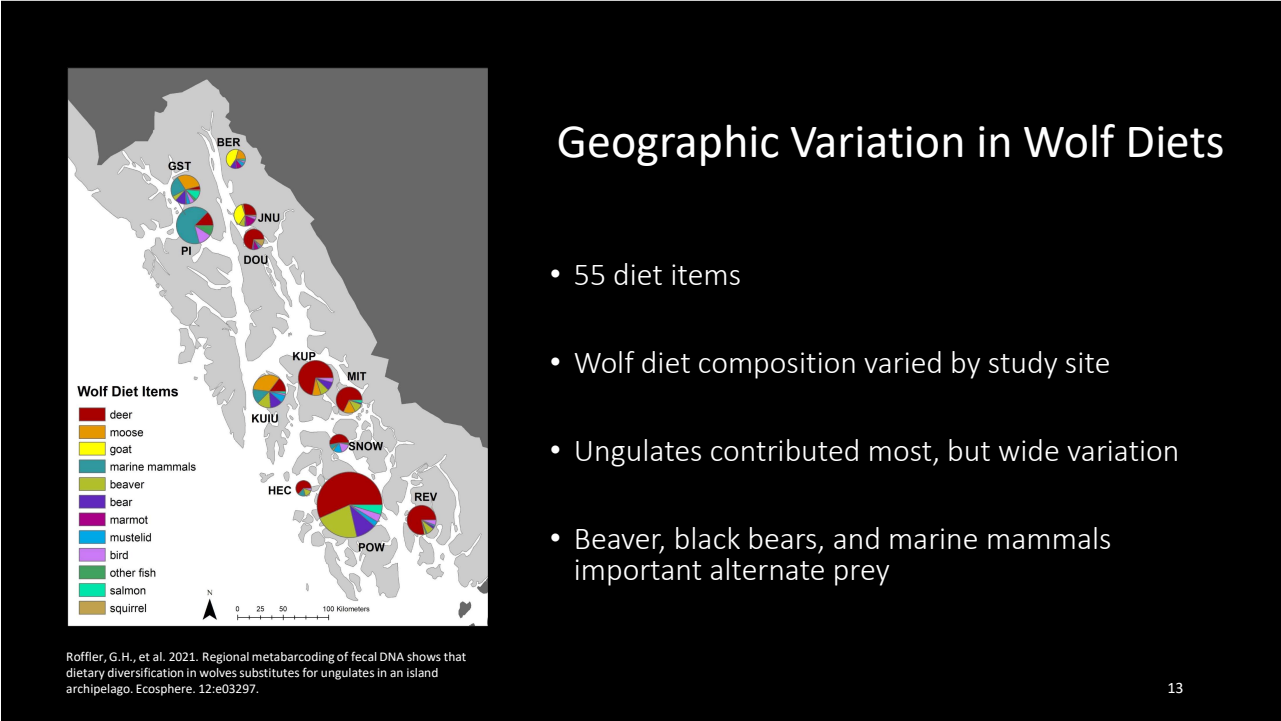
11

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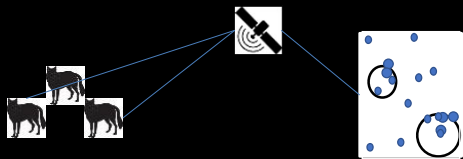
Photo: B. Dihle

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Seasonal Predation Patterns of Wolves

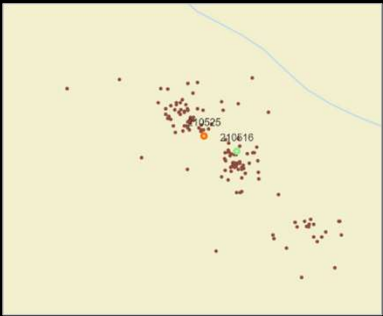
- Direct estimates of predation rates
- GPS collar locations every 30 minutes
- Estimation periods: Late summer, and late winter



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Seasonal Predation Patterns of Wolves



Photos: S. Neilson

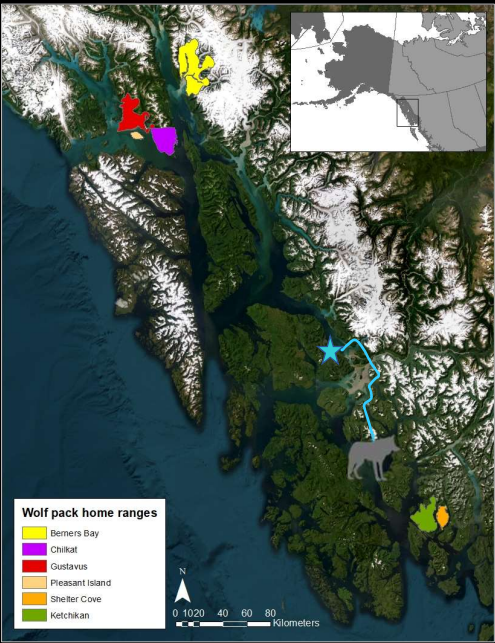
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Seasonal Predation Patterns of Wolves

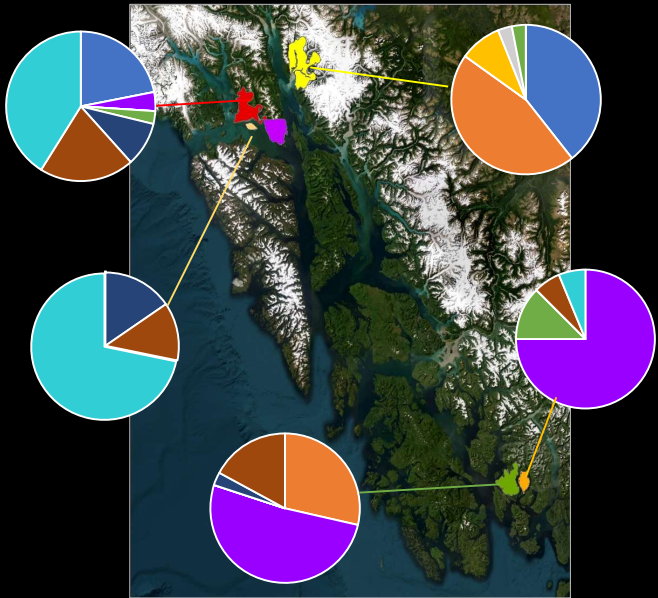
2018 – 2022

- 20 wolves instrumented
- 7 wolf packs, 4 study areas
- Average home range size = 384 km²



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Seasonal Predation Patterns of Wolves



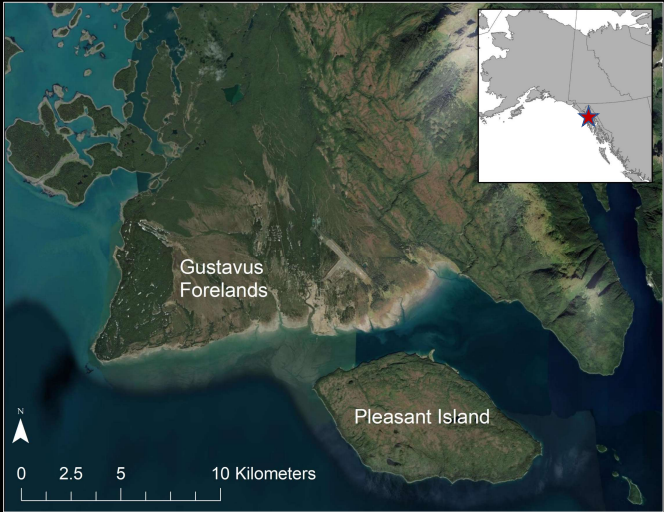
- 1,000 clusters investigated
- 172 kill sites
- 120 scavenging sites

- Moose
- Mountain goat
- Deer
- Sea otter
- Beaver
- Porcupine
- Bear
- Bird
- Salmon

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Seasonal Predation Patterns of Wolves



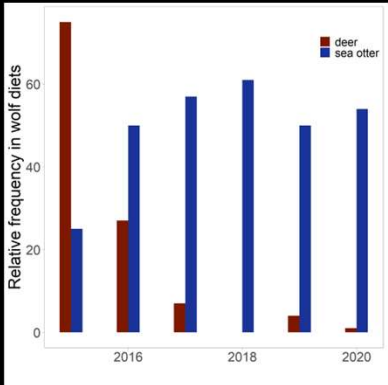
- 2013 wolves colonized Pleasant Island
- 50 km² island with 120–200 deer
- Gustavus – mainland system
- 3.9 moose/km²

Roffler, G.H., et al. In press. Recovery of a marine keystone predator transforms terrestrial predator-prey dynamics. PNAS.

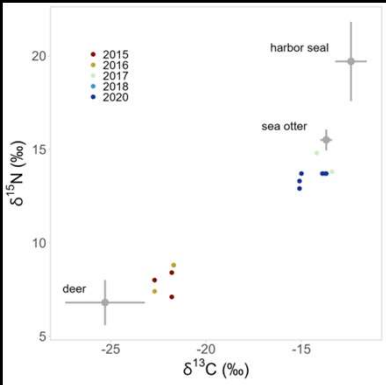
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Dietary shifts – Pleasant Island



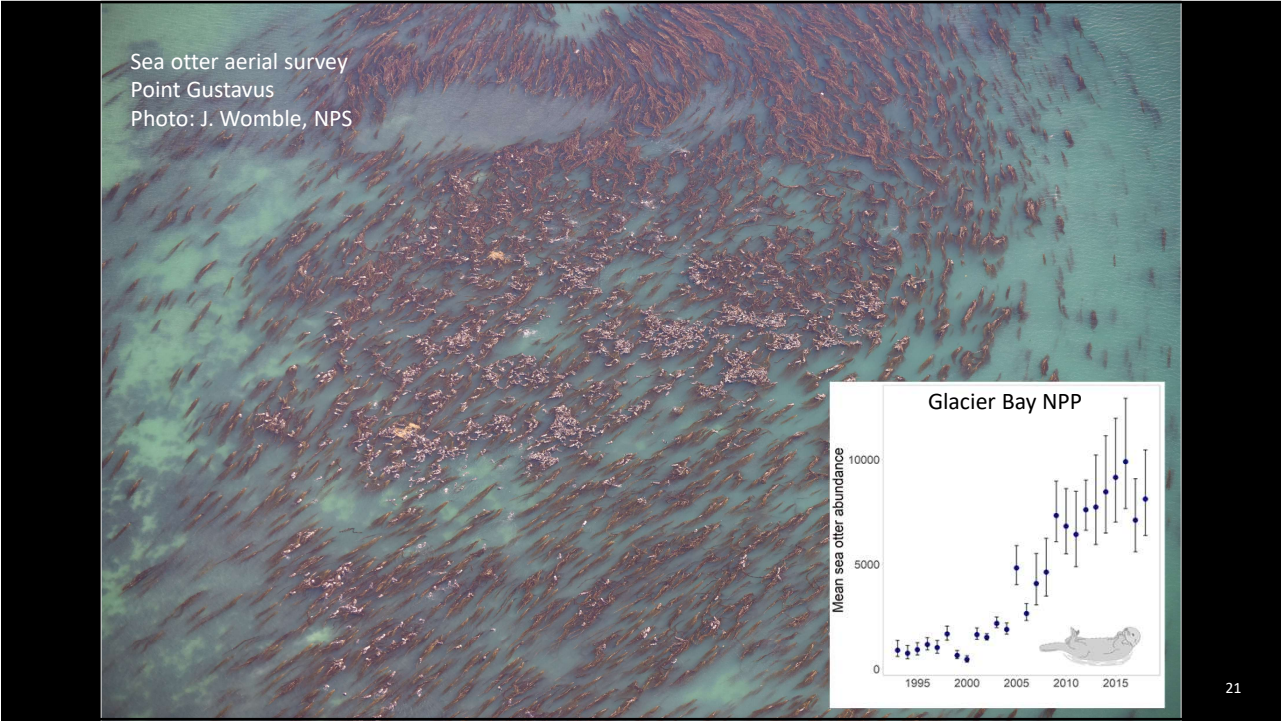
Fecal metabarcoding



Stable isotope ratios

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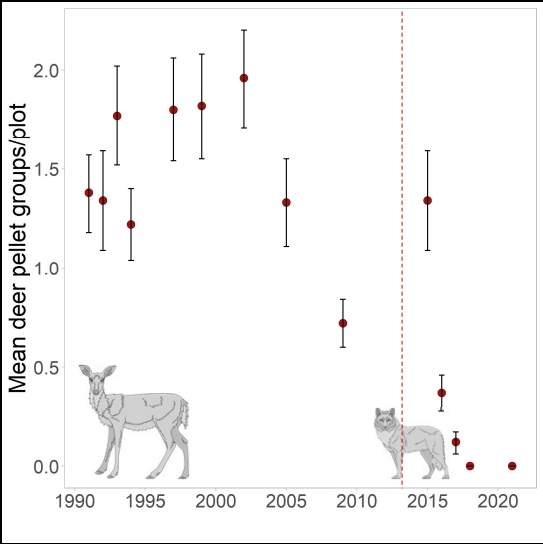
Wolf predation of sea otters

- Pleasant Island kill sites
- 30-day sessions, n = 3
- 26 wolf-killed sea otters
- 11 sea otters scavenged



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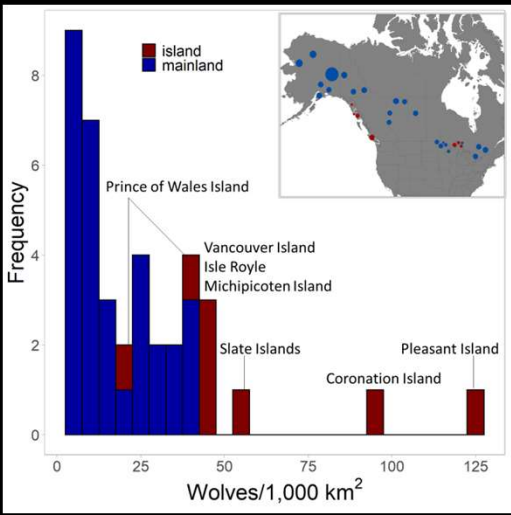
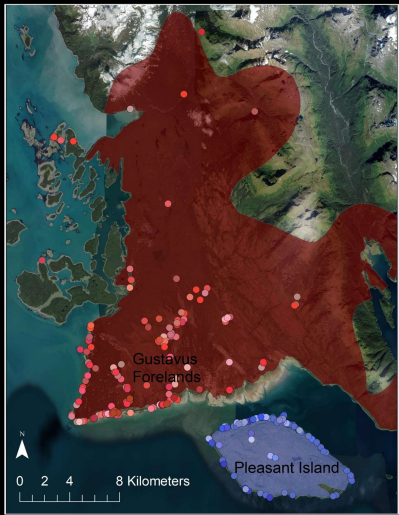
Deer abundance – Pleasant Island



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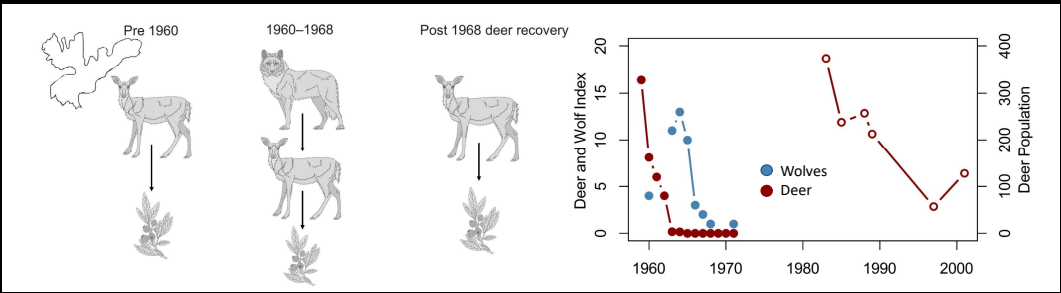
Wolf distribution and densities



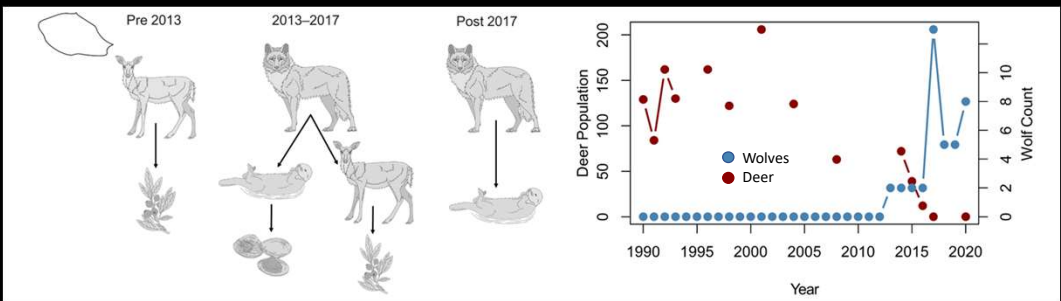
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Coronation Island



Pleasant Island



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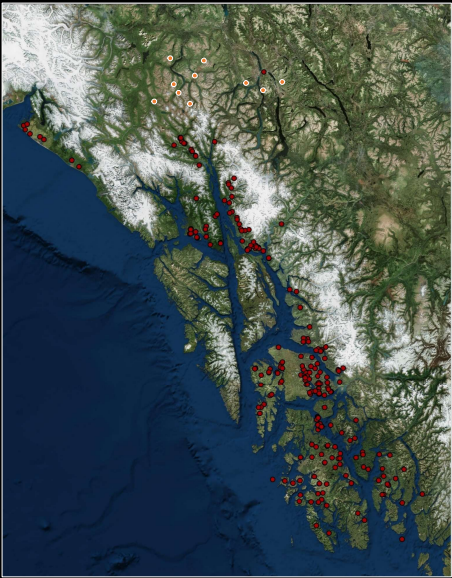
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Photo: B. Dihle


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Genetic Structure

- Identify isolated populations and areas of connectivity
- Define population boundaries
- Identify recent immigrants = gene flow
- ~600 samples
- ~37,000 SNPs



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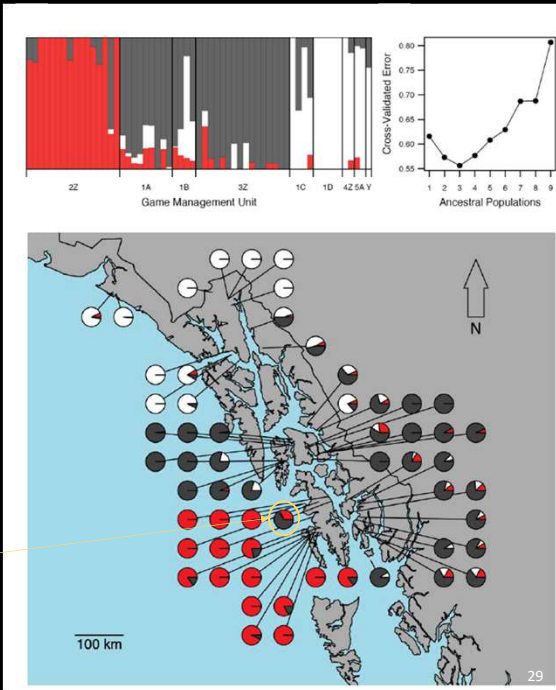
Genetic Structure

- 3 populations
- GMU2 distinct cluster
- Some evidence of admixture

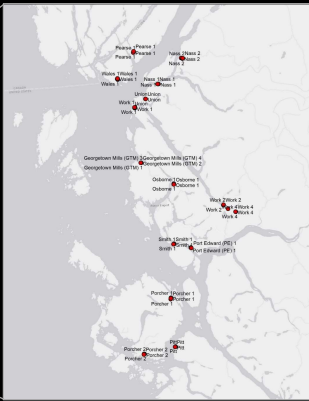
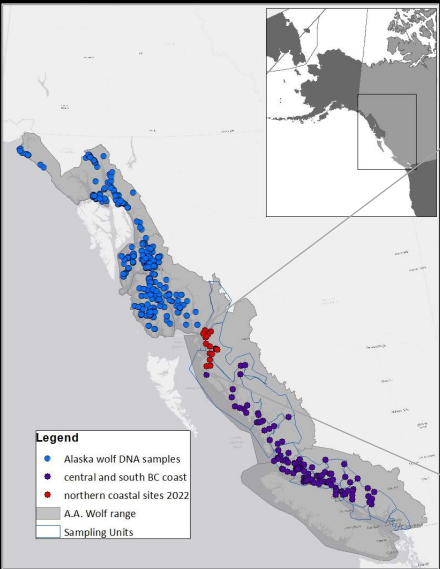
Wolf 201501



Zarn, K. et al. Genomic analysis of inbreeding in Alexander Archipelago wolves (*Canis lupus ligoni*). In review. Evolutionary Applications.



Genetic Structure – Range-wide A.A. Wolves



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Photo: B. Dihle

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Inbreeding

- Recent inbreeding in POW population
- More historically distant inbreeding in SE population

The figure consists of three scatter plots showing the proportion of the genome with runs of homozygosity (FROH) for four populations: POW, SE, NW, and IRNP. The y-axis represents FROH values from 0.0 to 1.0. The x-axis labels are POW, SE, NW, and IRNP. The three plots correspond to different genomic windows: FROH > 100 kb, FROH > 1 Mb, and FROH > 10 Mb. In the FROH > 100 kb plot, the POW population shows the highest values (median ~0.6), followed by SE (~0.5), NW (~0.4), and IRNP (~0.3). In the FROH > 1 Mb plot, the values are lower, with POW at ~0.3, SE at ~0.2, NW at ~0.1, and IRNP at ~0.1. In the FROH > 10 Mb plot, the values are the lowest, with POW at ~0.1, SE at ~0.05, NW at ~0.05, and IRNP at ~0.05. Error bars represent standard error.

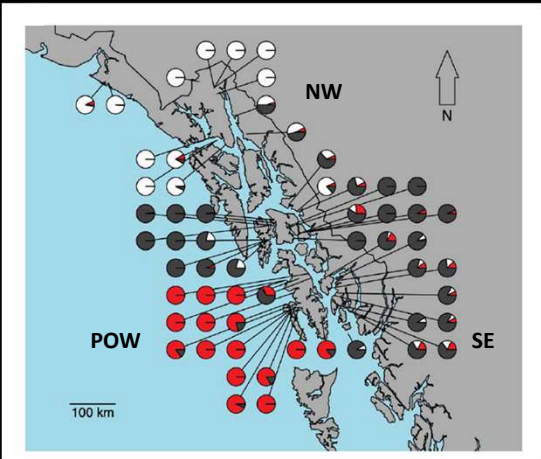
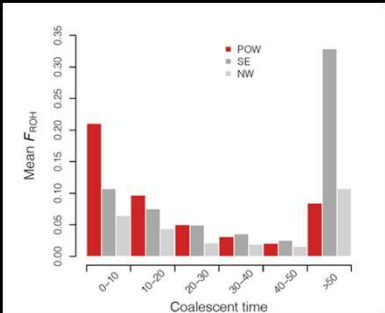
The map shows the study area, likely the Aleutian Islands, with sampling locations marked by colored circles. The circles are color-coded by population: POW (red), SE (black), NW (white), and IRNP (yellow). Lines connect the circles, indicating genetic relationships or gene flow. The map includes a scale bar for 100 km and a north arrow. The populations are labeled: POW (Pribilof Islands), SE (Sei Shoyan Islands), NW (Northwestern Islands), and IRNP (Irkutsk Islands).

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Inbreeding

- Inbreeding in POW 1970 - present
- Inbreeding in SE population ~ 1790



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Inbreeding

- Inbreeding depression = reduced fitness of individuals with related parents
- No evidence for reduction in fitness on POW
- Inbreeding depression very difficult to measure in natural populations
- Whole genome sequencing to measure accumulation of deleterious genetic variants
- Simulations – measure effects of migration on increasing genetic diversity



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